

GenCore version 4.5
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OM protein - protein search, using sw model

Run on:	September 4, 2002, 16:12:55 ; search time 101.54 Seconds			
Title:	US-09-052-089A-3			
Perfect score:	1066			
Sequence:	RTIINKLFFDIAQEEENVLDI.....DIQSADKEIMSIKKKLTMLQ 220			
Scoring table:	BLOSUM62			
Gappen:	10.0 , Gapext 0.5			
Searched:	283138 seqs, 96089334 residues			
Total number of hits satisfying chosen parameters:	283138			
Minimum DB seq length:	0			
Maximum DB seq length:	2000000000			
Post-processing:	Minimum Match 0%			
Database :	Maximum Match 100%			
	Listing first 45 summaries			
	PIR_711,* 1: Piri,* 2: pir2,* 3: pir3,* 4: pir4,*			
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	8			
SUMMARIES				
Result No.	Score	Query Length	DB ID	Description
1	530	49.7	433	T30807
2	170.5	16.0	1957	T38077
3	164.9	15.4	2116	A26655
4	163.5	15.3	1744	JH0720
5	161.1	15.1	1325	T42722
6	160.5	15.1	1938	A40997
7	160.5	15.1	1938	T30171
8	159.5	15.0	2139	T18295
9	159.4	14.9	1790	S67593
10	158.9	14.9	1935	S06006
11	156.5	14.7	959	A55913
12	156.5	14.7	1138	T24635
13	155.5	14.6	1017	PC4035
14	155.5	14.6	1164	T2805
15	155.5	14.6	1203	B55094
16	155.4	14.5	1938	A59293
17	155.4	14.5	1940	A24922
18	154.5	14.5	1509	A27224
19	154.4	14.4	1177	B75150
20	153.5	14.4	1133	T22976
21	152.5	14.3	579	JH0820
22	152.5	14.3	1935	A37102
23	152.5	14.3	1999	S21801
24	152	14.3	1175	C35815
25	152	14.3	1175	C35815
26	152	14.3	1201	A35815
27	152	14.3	1201	B35815
28	152	14.3	2385	A32491
29	14.3	2411	2	B32491

RESULT 1

Query Match Best local Similarity 49.7%; Score 530; DB 2; Length 433; Matches 104; Conservative 53; Mismatches 63; Indels 0; Gaps 0;

QY 1 RTIINKLFFDIAQEEENVLDI.....DIQSADKEIMSIKKKLTMLQ 220

Db 56 RHTISRLVFDVGDDSSYGDPESQNEDLRVYKVNFSKDRWKQKANDDLMEVELQ 115

QY 61 ATVAVSLOALGKAGMCLCSPLTKKKYQLEODDETRRAQAEGRURSKMKTMEQBLLOQ 120

Db 116 KALENLQKDVMKEKKLCSALRTQMTYLESQHNDTRAAKEEVRRURKMTFESLDVLQ 175

QY 121 QLEVEEEMTRDMGVGQSAVEQAVYCVSUKKEYENLKEARKASGEVADKLKDFFSRK 180

Db 176 QRAEVESMTDMGIGQAAYEQLSYCISLKEYDNLKGGLSSNMCERKLRREVLTSNK 235

QY 181 LQTVYSELDOAKLELKSQAOKDQSADKEMSLKKKLTMLQ 220

Db 236 LHKALLELTKARDQMSLQNDLTLNEKETSSLKKKVFHQ 275

RESULT 2

T38077 hypothetical coiled-coil protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C:Accession: T38077

R:Conor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.

submitted to the EMBL Data Library, April 1996

A:Reference number: 221767 ,

A:Accession: T38077

A:Status: preliminary; translated from GB/EMBL/DDJB

ALIGNMENTS

Total number of hits satisfying chosen parameters: 283138

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database : Maximum Match 100%

PIR_711,*
1: Piri,*
2: pir2,*
3: pir3,*
4: pir4,*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Query Match	Score	DB	Length
Best Local Similarity	15.3%	2;	1744;
Matches	25.8%	Pred. No.	0, 1;
60;	Conservative	Indels	39;
Mismatches	61;	Gaps	9;
Qy	12	AQBEEVNLDRPEELNDVRQLQSKDKEREDSOYLTIDTDLERNTAVLVSQALG	71
		: ; : ; : ; : ; : ; : ; : ; :	
Db	33	AALEEVN--ELLRKETHSLRSKSKSERCWKKKHHEEM-KLRLDAULDGHREMV-----	80
Qy	72	KAEMLCSTLKKOMKYLEQQDQTOKQOEEAGRLSRNMKTMEQIELLQLSQL-----P	123
::	::	:: : :: : : ; : ; : ; : ; : ; : ; :	
Db	81	QAEVMRDSIYEBIEFVKQRCLEEKQARADEKKELSESKKLLEETRAQINWLRKGOLEA	140
Qy	124	EVEEMIRDMGVQOSAVERQLAVCVSILKEYENLKEARKA--SGEVADKLK--DIFSS--	177
: ::		: ; : ; : ; : ; : ; : ; : ; :	
Db	141	ELEDILRDHEEKAALMEE--EIASFSQRLENFRVAPVAKPVEVDYAKLSETIWQAV	197
Qy	178	--RSKIQTVVSELDOKLEIKSAKD-----QSADKEIMSIRKKLMLQ	220
::	::	:: : ; : ; : ; : ; : ; : ; : ; :	
Db	198	EEYKSESVLEAGLSSESKENLRKVLEENKONRLLIQLSDKELVLISKMRKALE	250
RESULT	5		
T42722			
male-enhanced antigen-2 - mouse			
C:Species: Mus musculus (house mouse)			
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000			
C:Accession: T42722			
R.Kondo, M.; Sutou, S.			

A;accession: T42722
A;status: preliminary; translated from GB/EMBL/DDBJ
A;molecule type: mRNA
A;Residues: i-1325 <RQV>
A;cross-references: EMBL:D8270; NID:d1096175; PID:d1020389; PIDN:BAA19612.1
C;function: A;Experimental source: strain CD-1
C;description: supposed to play some role for spermatogenesis
C;keywords: leucine zipper

Query Match 15.1%; Score 161; DB 2; Length 1325;
Best Local Similarity 23.1%; Pred. No. 0.11; Mismatches 90; Indels 52; Gaps 7;
Matches 57; Conservative 48; Mismatches 90; Indels 52; Gaps 7;

Qy 13 QEEVNVLREFKLNEQ-----NVRQLSQDKKEKRDQSVIDTDLRDTLEENRATVSL 66
Db 956 REINSILATELAAREADYDVLQNLQVOAVLQRKEEDEKRDQMLQVQALQAFREKMEENSL 1025
C;accession: T30171
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
R;Buckson-Castaing, V.; Moudjou, M.; Ferguson, D.J.P.; Mucklow, M.; Belkaid, Y.; Mil
J. Cell Sci. 109, 179-190, 1996
A;title: Molecular characterisation of ninein, a new coiled-coil protein of the cent
A;reference number: 220751; Muid:96431720
A;Accession: T30171
A;status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-2168 <BOD>
A;Cross-references: EMBL:U0342; NID:91113864; PID:91113865; PIDN:AAA83234.1
A;Experimental source: strain C7B1/6
A;Note: localised specifically in the pericentriolar matrix of the centrosome

Db 1086 AQQTTELAAARTQDQ-----LIQKQL---DEQMSQOPTGSGEMEDLKWEELDKERIO 1135
Qy 155 NUKEARKASGEVADKLRLDFSSRSKLSQLOTVYSLDQAKLEKSRQDKLQSADKEIMSKR 214
Db 1136 SLQQLDQEPEQD---KIELEGQQTQIQTISKLEMVOEDLSSTOKDFMLQAKVELN 1192
Qy 215 KL-TMLQ 220
Db 1193 NMKFLLQ 1199

RESULT 6
A40997 myosin heavy chain, striated adductor muscle - scallop (Aequipecten irradians) N;Contains: Myosin ATPase (EC 3.6.1.32)
C;Species: Aequipecten irradians
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C;accession: A40997; S3557
R;Avitray, L.; Goodwin, E.B.; Szent-Groergyi, A.G.
J. Biol. Chem. 266, 18469-18476, 1991
A;Title: Complete primary structure of a scallop striated muscle myosin heavy chain. Seq
A;reference number: A40997; MUID:92011595
A;accession: A40997
A;molecule type: mRNA
A;residues: 1-1938 <NY1>
A;cross-references: GB:X5574; NID:95611; PIDN:CAA39247.1; PID:95612
C;superfamily: myosin heavy chain; myosin motor domain homology <NOT>
C;Keywords: actin binding; ATP; coiled coil; hydrolase; muscle contraction; nucleotide b
F;176-183/Region: nucleotide-binding motif A (P-loop)
F;547-586/Region: actin binding #status predicted
F;53-675/Region: actin binding #status predicted
F;136-1938/Region: S2
F;836-1276/Region: S2
F;1277-1938/Region: light meromyosin
F;82/Binding site: ATP (Lys) #status predicted
F;653,703/Active site: Cys #status predicted

Query Match 15.1%; Score 160.5; DB 1; Length 1938;
Best Local Similarity 28.1%; Pred. No. 0.17; Mismatches 56; Conservative 46; Mismatches 70; Indels 27; Gaps 7;

RESULT 8
T18296 myosin heavy chain - Entamoeba histolytica
C;Species: Entamoeba histolytica
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
C;accession: T18296
R;Guillen, N.
A;Reference number: Z18865
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2139 <GUT>
A;Cross-references: EMBL:L03534; NID:91850912; PID:91850913; PIDN:ABA48065.1
C;Genetics:
A;Gene: mhcA
C;Superfamily: myosin heavy chain; myosin motor domain homology

Db 1115 LEEBLEARNARAKVEKORAELENRELLEGLERDEAGG----ATSAQELNKKRE-AEL 1168
Db 1126 EEMIRDGMVGOSAVEQAVYCUSLKKYENLKEARKASGEVADKLRLDFSSRSKQTVY 185
Db 1159 LKIRRDL---EASLQEAQISALKRHQD-----ANENADQY-----DQLOVK 1211
Qy 186 SELDOQAKLELKSQAKDQS 204
Db 1212 SKLEKDQKDLKREMDDBLS 1230

F;91-780/domain: myosin motor domain homology <MMO>

Qy

Query Match 15.0%; Score 159.5; DB 2; Length 2139;

Best Local Similarity 24.0%; Pred. No. 0.21;

Matches 60; Conservative 49; Mismatches 96; Indels 45; Gaps 7;

Db

Qy

5 NKLFFDL-AQEENVLDREFLNLDRNVRQLSQRKDERKRSQVI-----ID 50
||: || : || : || | : || | : || | : || | : || | : || | : || |

Db

1144 NKIEDLRNMRQKIREKLDDBITKG - DV-SQYLOQKREYESQIAKMQKEERKIGNDKV 1200
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy

51 TLDTLEERNATVWSIQLQALGKAEMCSTLKKMKYLEDQQDDETRQAOSEAGRISKMT 110
| : | : | : || : | : | : | : | : | : | : | : | : | : | : |

Db

1201 NKEKTIKEKELEIPIOSLQEKIDTEVEKEDAEKKRKEIK--EMKALQEEKEVENESSKNS 1257
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy

111 MEQIELLQLSQPEVEEMIRDGMVGQSAVEQLAVCVSLKKEYENLKEARKASEVADL 170
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db

1258 TEKDOKKELNDKPDQKLUDDMTADNEKIKAKAOKDLEQNEVODNRHEKAVADLLNK 1317
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy

171 R---KDLFSSRKLQ-----TVYSELDOAKLELKSKDLSA 205
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db

1318 KAOSDKELNLSKAELEALTAKASVYESKNDSNEKAELSETOQANEKLNQADRKA 1377
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy

206 DKEIMSLKK 215
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |Db 1378 TADLQEAQEK 1387
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 9

RES

ULT

567593

transport protein US01 - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: Protein D255; protein YDL058w

C;Species: *Saccharomyces cerevisiae*

C;Accession: S67593; A38455; S30782

R;Bloecker, H.; Brandt, P.

submitted to the Protein Sequence Database, July 1996

A;Reference number: S67593

A;Cross-references: EMBL:Z74106; NID:91431058; PID:e253003; PID:91431059; MIPS:YDL058w

A;Molecule type: DNA

A;Residues: 1-1790 <BLO>

A;Experimental source: strain S288C

R;Nakajima, H.; Hirata, A.; Ogawa, Y.; Yonemura, T.; Yoda, K.; Yamasaki, M.

J. Cell Biol. 113, 245-260, 1991

A;Title: A cytoskeleton related gene, us01, is required for intracellular protein transp

A;Accession: A38455

A;Molecule type: DNA

A;Residues: 1-389 'A' 392-724, 'S' 726-1790 <NAK>

A;Cross references: GB:X54378; NID:94777; PID:94778

A;Note: the authors translated the codon ACT for residue 768 as Ile

R;Hossettler, M.K.; Herman, D.J.; Bendel, C.M.; McClellan, M.; Tao, N.; Kendrick, K.E.

submitted to the EMBL Data Library, February 1993

A;Description: An integrin analogue in *Saccharomyces cerevisiae*.

A;Reference number: S30782

A;Accession: S30782

A;Molecule type: DNA

A;Residues: 71-846 'E' 848-923 'K' 925-1252 'I' 1254-1318 'V' 1320-1460 'S' 1462-1580 'S'

A;Cross-references: EMBL:L03188

C;Genetics:

A;Gene: SGD:U501; INT1

A;Cross references: SGD:S0002216; MIPS:YDL058w

A;Map position: 4L

C;Keywords: coiled coil; transmembrane protein

F;326-342/Domain: transmembrane #status predicted <TM1>

F;344-410/Domain: transmembrane #status predicted <TM2>

F;617-633/Domain: transmembrane #status predicted <TM3>

Qy

1 RTIINKLFLDLAQ---EERVLDRFLK-----NELDNTRAQLSQCDKRDQSVI 48
| : ; : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db 1369 RKLINEGSSTITOYESEKINTLDELIRI-QNENELKAKEIDNTSEL-EKVLSND--- 1423

Db

1424 -----ELLEBEKONTIKSLODEILSYDKITRNDEKLLSIERDKRDLESSKEOLRANES 1478

Qy

49 IDTDRDTLERNATVWSIQLQALGKAEMCSTLKKMKYLEDQQDDETRQAOSEAGRISKMT 110
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db

101 AGRURSKMTIMEQFELLOSQLPVEEMIRDGMVGQSAVE---QLAVCVSLKKEYENL 156
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy

1479 KAKYEEGLKLKEESESSKEALELKSKMML--ESTESNETELKSMETTRKSDEKL 1535
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db

157 KEARKASGEVADLR-----KDLFSSRKLQTV--SELDQAKLELKSAQ 199
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy

1535 EOSKSAEDIQNQHEKSDLSRINESKDIELKSKRIEAKSGSELETVKOELNNQ 1595
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db

1596 EKIRINAEPNTVLKSKL 1612
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Qy

200 KDQOSADKEMISLKKL 216
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Db

S06006 myosin beta heavy chain, cardiac muscle [similarity] - rat
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

N;Contains: myosin ATPase (EC 3.6.1.32)

C;Species: *Rattus norvegicus* (Norway rat)

C;Accession: S06006; S07536; I6741; A02989

R;Kraft, R.; Bravo-Zehnder, M.; Taylor, D.A.; Leinwand, L.A.

Nucleic Acids Res. 17, 7529-7530, 1989

A;Title: Complete nucleotide sequence of full length cDNA for rat beta cardiac myosin

A;Reference number: S06006; MUID:90016823

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-1935 <KRA>

A;Cross references: EMBL:15939; NID:956656; PID:CAA34065..1; PID:956657

R;McNamee, E.M.; Kraft, R.; Bravo-Zehnder, M.; Taylor, D.A.; Leinwand, L.A.

J. Mol. Biol. 210, 665-671, 1989

A;Title: Full-length rat alpha and beta cardiac myosin heavy chain sequences. Compari

A;Reference number: S07535; MUID:90133919

A;Accession: S07536

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-950 'RK' 953-1935 <MCN>

R;Mahdavi, V.; Lompre, A.M.; Chambers, A.P.; Nadal-Ginard, B.

EUR. Heart J. 5, 181-191, 1984

A;Title: Cardiac myosin heavy chain isozymic transitions during development and under

A;Reference number: I5305; MUID:85179510

A;Accession: I67441

A;Status: translated from GB/EMBL/DDJB

A;Molecule type: mRNA

A;Residues: 1871-1935 <RES>

A;Cross references: GB:N32698; NID:9205598; PID:AAA41659..1; PID:9205599

R;Mahdavi, V.; Periasamy, M.; Nadal-Ginard, B.

Nature 297, 659-666, 1982

A;Title: Molecular characterization of two myosin heavy chain genes expressed in the

A;Reference number: A02988; MUID:82220036

A;Accession: A02989

A;Molecule type: mRNA

A;Residues: 1524-1528 'V' 1530 'R' 1532-1730 'H' 1732-1783 'K' 1785-1850 'N' 1852-185

A;Cross references: GB:X00722; NID:9205577; PID:AAA1654..1; PID:9205578

C;Superfamily: myosin heavy chain; myosin motor domain homology

C;Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methyl

F;88-766/Domain: myosin motor domain homology <MMOT>

F;78-185/Region: nucleotide-binding motif A (P-loop)

F;58-58/Region: actin binding #status predicted

F;55-67/Region: actin binding #status predicted

F;839-1935/Domain: coiled coil #status predicted <COI>

F;839-1279/Region: S2

F;129/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted

Query Match 14.9%; Score 159; DB 2; Length 1790;
Best Local Similarity 23.7%; Pred. No. 0.19;
Matches 61; Conservative 57; Mismatches 85; Indels 54; Gaps 9;

F;184/Binding site: ATP (Lys) #status predicted
F;695,705/Active site: Cys #status predicted

Db 900 TDSKKEQDDLLVILADQQKILSLKSKL 927

Query Match 14.9%; Score 158.5; DB 1; Length 1935;
Best Local Similarity 20.8%; Pred. No. 22; Mismatches 87; Indels 89; Gaps 9;
Matches 62; Conservative 60; Mismatches 87; Indels 89; Gaps 9;

Qy 1 RTINKLKFDDLAQEENYVLDR-----ERIK----- 25
Db 1129 RAKVEKLRSLSLSEERLBBAGGATSVQEMNKREAEFQKMRDLEETLQHEAT 1188
Qy 26 -----NELDNVRAQLSOKDKERDSQVITDTRTLDEERNATVVSQQA 69
Db 1189 AAALRKKHADSVAELGEIDNQILOVKOKKEKESEKFLDDTSNMQ----- 1241
Qy 70 LGKAKMCLGSTLKQMKYLFQQQDTKQAOEEACRLRSKMT-----MEQIELLQSQ 121
Db 1242 KANLKEMCRTLEDOMNEHRSKAETORSVNDLTQRAKLQTENGELSRLDEREALI-SQ 1300
Qy 122 LP-----EVEMMRDMCGYQGSAYEQLAVYCYSKKEYENLKARKASGV 166
Db 1301 LTRGKLYTYQOLEDLKRROLEEVAKNALAHALQSARHDCDLIREQEETEAKAELQY 1360
Qy 167 ADKURKDLESSRKLQT---VISELDOAKLEKSAQKDLSADKEIMSLKKLMLQ 220
Db 1361 LSKANSEVAQWRTKYETDAIQTEEEAKKL-AQRLQDAAEVEAVNAKCSSL 1415

RESULT 11

A55913

transcytosis associated protein p115 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 05-Nov-1999
C;Accession: A55913
R;Barroso, M.; Nelson, D.S.; Sztil, E. 1995
PROC. NATL. ACAD. SCI. U.S.A. 92, 527-531, 1995
A;Title: Transcytosis-associated protein (TAP)/p115 is a general fusion factor required
A;Reference number: A55913; MUID:95132633
A;Accession: A55913
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-959 <BAR>
A;Cross-references: GB:U15589; NID:9558474; PIDN:AAC52151.1; PID:9558475
C;Keywords: membrane fusion; membrane trafficking

RESULT 12

A55913

Query Match 14.7%; Score 156.5; DB 2; Length 1138;
Best Local Similarity 24.7%; Pred. No. 0.16; Mismatches 58; Conservative 45; Mismatches 73; Indels 59; Gaps 9;
Matches 66; Conservative 53; Mismatches 78; Indels 131; Gaps 9;

Qy 1 RTINKLKFDDLAQEENYVLDREF-LKNEVDNRAQL-----SOKDKER 43
Db 544 KTIVKNTY-LSESQKVYLESEINLNKNDMAEVKLNRNSOHQVAGLNEKISEEKRKQ 602
Qy 44 DSQVITDTRTLDEERNATVVSQQLGKAEML--CSTLKKQMKYLFQQQDTKQAOEEA 101
Db 603 DADV-----TRLDQNOKL-LREAQDSAELEEVEQKGKREIDLHQLQAHOSSEGSV 654
Qy 102 GRURSKMKMPEELLQSQQLQPEVEMDRDMCGYQGSAYEQLAVYCYSKKEYENLKARK 161
Db 655 GOLOOKLASEHREHYLQLELERVMKMERD-----LDGRILEGYIRSEA 697

RESULT 13

A55913

Query Match 14.7%; Score 156.5; DB 2; Length 1138;
Best Local Similarity 24.7%; Pred. No. 0.16; Mismatches 58; Conservative 45; Mismatches 73; Indels 59; Gaps 9;
Matches 66; Conservative 53; Mismatches 78; Indels 131; Gaps 9;

Qy 71 GKAEMLCSTLKKQMKYLFQQQDE-----TKQAK----- 98
Db 660 REQDQOLEELKQVQSTLKQNEQDQIATVQHQAKQHQDQYVNLKVOLGKDHHQGSHS 719
Qy 99 -----EEAGRLRSKMTQMOIELLIQSQLPVEPEMIRN-----GVOSAV-- 139
Db 720 DGAQVNGIOPPEEISRLREEELRSHQVLIQSQLAEKOTVIENRSSQVSGMSQALATC 779
Qy 140 -----EQAVV----- 145
Db 780 SPRDAAEQVELKQELSAKSQCSQSLEITRLQTENRELQRAETLAKSVPVGESELVT 839
Qy 146 -----CVSLKKEYENLKEARKASGEVAKLKRDLFSSRSKLTQVYSELQAKEL 195
Db 840 AAKITDVGEVLSSALQETKELKNEKIALKSEERTSIQQLDSSNSTIAIQLQTERDKLYEV 899
Qy 196 KSAQKD-----LQSADKEIMSLKKL 216

RESULT 14

A55913

Query Match 14.7%; Score 156.5; DB 2; Length 1138;
Best Local Similarity 24.7%; Pred. No. 0.16; Mismatches 58; Conservative 45; Mismatches 73; Indels 59; Gaps 9;
Matches 66; Conservative 53; Mismatches 78; Indels 131; Gaps 9;

Qy 71 GKAEMLCSTLKKQMKYLFQQQDE-----TKQAK----- 98
Db 660 REQDQOLEELKQVQSTLKQNEQDQIATVQHQAKQHQDQYVNLKVOLGKDHHQGSHS 719
Qy 99 -----EEAGRLRSKMTQMOIELLIQSQLPVEPEMIRN-----GVOSAV-- 139
Db 720 DGAQVNGIOPPEEISRLREEELRSHQVLIQSQLAEKOTVIENRSSQVSGMSQALATC 779
Qy 140 -----EQAVV----- 145
Db 780 SPRDAAEQVELKQELSAKSQCSQSLEITRLQTENRELQRAETLAKSVPVGESELVT 839
Qy 146 -----CVSLKKEYENLKEARKASGEVAKLKRDLFSSRSKLTQVYSELQAKEL 195
Db 840 AAKITDVGEVLSSALQETKELKNEKIALKSEERTSIQQLDSSNSTIAIQLQTERDKLYEV 899
Qy 196 KSAQKD-----LQSADKEIMSLKKL 216

RESULT 15

A55913

Query Match 14.7%; Score 156.5; DB 2; Length 1138;
Best Local Similarity 24.7%; Pred. No. 0.16; Mismatches 58; Conservative 45; Mismatches 73; Indels 59; Gaps 9;
Matches 66; Conservative 53; Mismatches 78; Indels 131; Gaps 9;

Qy 71 GKAEMLCSTLKKQMKYLFQQQDE-----TKQAK----- 98
Db 660 REQDQOLEELKQVQSTLKQNEQDQIATVQHQAKQHQDQYVNLKVOLGKDHHQGSHS 719
Qy 99 -----EEAGRLRSKMTQMOIELLIQSQLPVEPEMIRN-----GVOSAV-- 139
Db 720 DGAQVNGIOPPEEISRLREEELRSHQVLIQSQLAEKOTVIENRSSQVSGMSQALATC 779
Qy 140 -----EQAVV----- 145
Db 780 SPRDAAEQVELKQELSAKSQCSQSLEITRLQTENRELQRAETLAKSVPVGESELVT 839
Qy 146 -----CVSLKKEYENLKEARKASGEVAKLKRDLFSSRSKLTQVYSELQAKEL 195
Db 840 AAKITDVGEVLSSALQETKELKNEKIALKSEERTSIQQLDSSNSTIAIQLQTERDKLYEV 899
Qy 196 KSAQKD-----LQSADKEIMSLKKL 216

RESULT 16

A55913

Query Match 14.7%; Score 156.5; DB 2; Length 1138;
Best Local Similarity 24.7%; Pred. No. 0.16; Mismatches 58; Conservative 45; Mismatches 73; Indels 59; Gaps 9;
Matches 66; Conservative 53; Mismatches 78; Indels 131; Gaps 9;

Qy 71 GKAEMLCSTLKKQMKYLFQQQDE-----TKQAK----- 98
Db 660 REQDQOLEELKQVQSTLKQNEQDQIATVQHQAKQHQDQYVNLKVOLGKDHHQGSHS 719
Qy 99 -----EEAGRLRSKMTQMOIELLIQSQLPVEPEMIRN-----GVOSAV-- 139
Db 720 DGAQVNGIOPPEEISRLREEELRSHQVLIQSQLAEKOTVIENRSSQVSGMSQALATC 779
Qy 140 -----EQAVV----- 145
Db 780 SPRDAAEQVELKQELSAKSQCSQSLEITRLQTENRELQRAETLAKSVPVGESELVT 839
Qy 146 -----CVSLKKEYENLKEARKASGEVAKLKRDLFSSRSKLTQVYSELQAKEL 195
Db 840 AAKITDVGEVLSSALQETKELKNEKIALKSEERTSIQQLDSSNSTIAIQLQTERDKLYEV 899
Qy 196 KSAQKD-----LQSADKEIMSLKKL 216

RESULT 17

A55913

Query Match 14.7%; Score 156.5; DB 2; Length 1138;
Best Local Similarity 24.7%; Pred. No. 0.16; Mismatches 58; Conservative 45; Mismatches 73; Indels 59; Gaps 9;
Matches 66; Conservative 53; Mismatches 78; Indels 131; Gaps 9;

Qy 71 GKAEMLCSTLKKQMKYLFQQQDE-----TKQAK----- 98
Db 660 REQDQOLEELKQVQSTLKQNEQDQIATVQHQAKQHQDQYVNLKVOLGKDHHQGSHS 719
Qy 99 -----EEAGRLRSKMTQMOIELLIQSQLPVEPEMIRN-----GVOSAV-- 139
Db 720 DGAQVNGIOPPEEISRLREEELRSHQVLIQSQLAEKOTVIENRSSQVSGMSQALATC 779
Qy 140 -----EQAVV----- 145
Db 780 SPRDAAEQVELKQELSAKSQCSQSLEITRLQTENRELQRAETLAKSVPVGESELVT 839
Qy 146 -----CVSLKKEYENLKEARKASGEVAKLKRDLFSSRSKLTQVYSELQAKEL 195
Db 840 AAKITDVGEVLSSALQETKELKNEKIALKSEERTSIQQLDSSNSTIAIQLQTERDKLYEV 899
Qy 196 KSAQKD-----LQSADKEIMSLKKL 216

RESULT 18

A55913

Query Match 14.7%; Score 156.5; DB 2; Length 1138;
Best Local Similarity 24.7%; Pred. No. 0.16; Mismatches 58; Conservative 45; Mismatches 73; Indels 59; Gaps 9;
Matches 66; Conservative 53; Mismatches 78; Indels 131; Gaps 9;

Qy 71 GKAEMLCSTLKKQMKYLFQQQDE-----TKQAK----- 98
Db 660 REQDQOLEELKQVQSTLKQNEQDQIATVQHQAKQHQDQYVNLKVOLGKDHHQGSHS 719
Qy 99 -----EEAGRLRSKMTQMOIELLIQSQLPVEPEMIRN-----GVOSAV-- 139
Db 720 DGAQVNGIOPPEEISRLREEELRSHQVLIQSQLAEKOTVIENRSSQVSGMSQALATC 779
Qy 140 -----EQAVV----- 145
Db 780 SPRDAAEQVELKQELSAKSQCSQSLEITRLQTENRELQRAETLAKSVPVGESELVT 839
Qy 146 -----CVSLKKEYENLKEARKASGEVAKLKRDLFSSRSKLTQVYSELQAKEL 195
Db 840 AAKITDVGEVLSSALQETKELKNEKIALKSEERTSIQQLDSSNSTIAIQLQTERDKLYEV 899
Qy 196 KSAQKD-----LQSADKEIMSLKKL 216

RESULT 19

A55913

Query Match 14.7%; Score 156.5; DB 2; Length 1138;
Best Local Similarity 24.7%; Pred. No. 0.16; Mismatches 58; Conservative 45; Mismatches 73; Indels 59; Gaps 9;
Matches 66; Conservative 53; Mismatches 78; Indels 131; Gaps 9;

Qy 71 GKAEMLCSTLKKQMKYLFQQQDE-----TKQAK----- 98
Db 660 REQDQOLEELKQVQSTLKQNEQDQIATVQHQAKQHQDQYVNLKVOLGKDHHQGSHS 719
Qy 99 -----EEAGRLRSKMTQMOIELLIQSQLPVEPEMIRN-----GVOSAV-- 139
Db 720 DGAQVNGIOPPEEISRLREEELRSHQVLIQSQLAEKOTVIENRSSQVSGMSQALATC 779
Qy 140 -----EQAVV----- 145
Db 780 SPRDAAEQVELKQELSAKSQCSQSLEITRLQTENRELQRAETLAKSVPVGESELVT 839
Qy 146 -----CVSLKKEYENLKEARKASGEVAKLKRDLFSSRSKLTQVYSELQAKEL 195
Db 840 AAKITDVGEVLSSALQETKELKNEKIALKSEERTSIQQLDSSNSTIAIQLQTERDKLYEV 899
Qy 196 KSAQKD-----LQSADKEIMSLKKL 216

RESULT 20

A55913

Query Match 14.7%; Score 156.5; DB 2; Length 1138;
Best Local Similarity 24.7%; Pred. No. 0.16; Mismatches 58; Conservative 45; Mismatches 73; Indels 59; Gaps 9;
Matches 66; Conservative 53; Mismatches 78; Indels 131; Gaps 9;

Qy 71 GKAEMLCSTLKKQMKYLFQQQDE-----TKQAK----- 98
Db 660 REQDQOLEELKQVQSTLKQNEQDQIATVQHQAKQHQDQYVNLKVOLGKDHHQGSHS 719
Qy 99 -----EEAGRLRSKMTQMOIELLIQSQLPVEPEMIRN-----GVOSAV-- 139
Db 720 DGAQVNGIOPPEEISRLREEELRSHQVLIQSQLAEKOTVIENRSSQVSGMSQALATC 779
Qy 140 -----EQAVV----- 145
Db 780 SPRDAAEQVELKQELSAKSQCSQSLEITRLQTENRELQRAETLAKSVPVGESELVT 839
Qy 146 -----CVSLKKEYENLKEARKASGEVAKLKRDLFSSRSKLTQVYSELQAKEL 195
Db 840 AAKITDVGEVLSSALQETKELKNEKIALKSEERTSIQQLDSSNSTIAIQLQTERDKLYEV 899
Qy 196 KSAQKD-----LQSADKEIMSLKKL 216

RESULT 21

A55913

Query Match 14.7%; Score 156.5; DB 2; Length 1138;
Best Local Similarity 24.7%; Pred. No. 0.16; Mismatches 58; Conservative 45; Mismatches 73; Indels 59; Gaps 9;
Matches 66; Conservative 53; Mismatches 78; Indels 131; Gaps 9;

Qy 71 GKAEMLCSTLKKQMKYLFQQQDE-----TKQAK----- 98
Db 660 REQDQOLEELKQVQSTLKQNEQDQIATVQHQAKQHQDQYVNLKVOLGKDHHQGSHS 719
Qy 99 -----EEAGRLRSKMTQMOIELLIQSQLPVEPEMIRN-----GVOSAV-- 139
Db 720 DGAQVNGIOPPEEISRLREEELRSHQVLIQSQLAEKOTVIENRSSQVSGMSQALATC 779
Qy 140 -----EQAVV----- 145
Db 780 SPRDAAEQVELKQELSAKSQCSQSLEITRLQTENRELQRAETLAKSVPVGESELVT 839
Qy 146 -----CVSLKKEYENLKEARKASGEVAKLKRDLFSSRSKLTQVYSELQAKEL 195
Db 840 AAKITDVGEVLSSALQETKELKNEKIALKSEERTSIQQLDSSNSTIAIQLQTERDKLYEV 899
Qy 196 KSAQKD-----LQSADKEIMSLKKL 216

RESULT 22

A55913

Query Match 14.7%; Score 156.5; DB 2; Length 1138;
Best Local Similarity 24.7%; Pred. No. 0.16; Mismatches 58; Conservative 45; Mismatches 73; Indels 59; Gaps 9;
Matches 66; Conservative 53; Mismatches 78; Indels 131; Gaps 9;

Qy 71 GKAEMLCSTLKKQMKYLFQQQDE-----TKQAK----- 98
Db 660 REQDQOLEELKQVQSTLKQNEQDQIATVQHQAKQHQDQYVNLKVOLGKDHHQGSHS 719
Qy 99 -----EEAGRLRSKMTQMOIELLIQSQLPVEPEMIRN-----GVOSAV-- 139
Db 720 DGAQVNGIOPPEEISRLREEELRSHQVLIQSQLAEKOTVIENRSSQVSGMSQALATC 779
Qy 140 -----EQAVV----- 145
Db 780 SPRDAAEQVELKQELSAKSQCSQSLEITRLQTENRELQRAETLAKSVPVGESELVT 839
Qy 146 -----CVSLKKEYENLKEARKASGEVAKLKRDLFSSRSKLTQVYSELQAKEL 195
Db 840 AAKITDVGEVLSSALQETKELKNEKIALKSEERTSIQQLDSSNSTIAIQLQTERDKLYEV 899
Qy 196 KSAQKD-----LQSADKEIMSLKKL 216

RESULT 23

A55913

Query Match 14.7%; Score 156.5; DB 2; Length 1138;
Best Local Similarity 24.7%; Pred. No. 0.16; Mismatches 58; Conservative 45; Mismatches 73; Indels 59; Gaps 9;
Matches 66; Conservative 53; Mismatches 78; Indels 131; Gaps 9;

Qy 71 GKAEMLCSTLKKQMKYLFQQQDE-----TKQAK----- 98
Db 660 REQDQOLEELKQVQSTLKQNEQDQIATVQHQAKQHQDQYVNLKVOLGKDHHQGSHS 719
Qy 99 -----EEAGRLRSKMTQMOIELLIQSQLPVEPEMIRN-----GVOSAV-- 139
Db 720 DGAQVNGIOPPEEISRLREEELRSHQVLIQSQLAEKOTVIENRSSQVSGMSQALATC 779
Qy 140 -----EQAVV----- 145
Db 780 SPRDAAEQVELKQELSAKSQCSQSLEITRLQTENRELQRAETLAKSVPVGESELVT 839
Qy 146 -----CVSLKKEYENLKEARKASGEVAKLKRDLFSSRSKLTQVYSELQAKEL 195
Db 840 AAKITDVGEVLSSALQETKELKNEKIALKSEERTSIQQLDSSNSTIAIQLQTERDKLYEV 899
Qy 196 KSAQKD-----LQSADKEIMSLKKL 216

RESULT 24

A55913

Query Match 14.7%; Score 156.5; DB 2; Length 1138;
Best Local Similarity 24.7%; Pred. No. 0.16; Mismatches 58; Conservative 45; Mismatches 73; Indels 59; Gaps 9;
Matches 66; Conservative 53; Mismatches 78; Indels 131; Gaps 9;

Qy 71 GKAEMLCSTLKKQMKYLFQQQDE-----TKQAK----- 98
Db 660 REQDQOLEELKQVQSTLKQNEQDQIATVQHQAKQHQDQYVNLKVOLGKDHHQGSHS 719
Qy 99 -----EEAGRLRSKMTQMOIELLIQSQLPVEPEMIRN-----GVOSAV-- 139
Db 720 DGAQVNGIOPPEEISRLREEELRSHQVLIQSQLAEKOTVIENRSSQVSGMSQALATC 779
Qy 140 -----EQAVV----- 145
Db 780 SPRDAAEQVELKQELSAKSQCSQSLEITRLQTENRELQRAETLAKSVPVGESELVT 839
Qy 146 -----CVSLKKEYENLKEARKASGEVAKLKRDLFSSRSKLTQVYSELQAKEL 195
Db 840 AAKITDVGEVLSSALQETKELKNEKIALKSEERTSIQQLDSSNSTIAIQLQTERDKLYEV 899
Qy 196 KSAQKD-----LQSADKEIMSLKKL 216

RESULT 25

A55913

Query Match 14.7%; Score 156.5; DB 2; Length 1138;
Best Local Similarity 24.7%; Pred. No. 0.16; Mismatches 58; Conservative 45; Mismatches 73; Indels 59; Gaps 9;
Matches 66; Conservative 53; Mismatches 78; Indels 131; Gaps 9;

Qy 71 GKAEMLCSTLKKQMKYLFQQQDE-----TKQAK----- 98
Db 660 REQDQOLEELKQVQSTLKQNEQDQIATVQHQAKQHQDQYVNLKVOLGKDHHQGSHS 719
Qy 99 -----EEAGRLRSKMTQMOIELLIQSQLPVEPEMIRN-----GVOSAV-- 139
Db 720 DGAQVNGIOPPEEISRLREEELRSHQVLIQSQLAEKOTVIENRSSQVSGMSQALATC 779
Qy 140 -----EQAVV----- 145
Db 780 SPRDAAEQVELKQELSAKSQCSQSLEITRLQTENRELQRAETLAKSVPVGESELVT 839
Qy 146 -----CVSLKKEYENLKEARKASGEVAKLKRDLFSSRSKLTQVYSELQAKEL 195
Db 840 AAKITDVGEVLSSALQETKELKNEKIALKSEERTSIQQLDSSNSTIAIQLQTERDKLYEV 899
Qy 196 KSAQKD-----LQSADKEIMSLKKL 216

RESULT 26

A55913

Query Match 14.7%; Score 156.5; DB 2; Length 1138;
Best Local Similarity 24.7%; Pred. No. 0.16; Mismatches 58; Conservative 45; Mismatches 73; Indels 59; Gaps 9;
Matches 66; Conservative 53; Mismatches 78; Indels 131; Gaps 9;

Qy 71 GKAEMLCSTLKKQMKYLFQQQDE-----TKQAK----- 98
Db 660 REQDQOLEELKQVQSTLKQNEQDQIATVQHQAKQHQDQYVNLKVOLGKDHHQGSHS 719
Qy 99 -----EEAGRLRSKMTQMOIELLIQSQLPVEPEMIRN-----GVOSAV-- 139
Db 720 DGAQVNGIOPPEEISRLREEELRSHQVLIQSQLAEKOTVIENRSSQVSGMSQALATC 779
Qy 140 -----EQAVV----- 145
Db 780 SPRDAAEQVELKQELSAKSQCSQSLEITRLQTENRELQRAETLAKSVPVGESELVT 839
Qy 146 -----CVSLKKEYENLKEARKASGEVAKLKRDLFSSRSKLTQVYSELQAKEL 195
Db 840 AAKITDVGEVLSSALQETKELKNEKIALKSEERTSIQQLDSSNSTIAIQLQTERDKLYEV 899
Qy 196 KSAQKD-----LQSADKEIMSLKKL 216

RESULT 27

A55913

Query Match 14.7%; Score 156.5; DB 2; Length 1138;
Best Local Similarity 24.7%; Pred. No. 0.16; Mismatches 58; Conservative 45; Mismatches 73; Indels 59; Gaps 9;
Matches 66; Conservative 53; Mismatches 78; Indels 131; Gaps 9;

Qy 71 GKAEMLCSTLKKQMKYLFQQQDE-----TKQAK----- 98
Db 660 REQDQOLEELKQVQSTLKQNEQDQIATVQHQAKQHQDQYVNLKVOLGKDHHQGSHS 719
Qy 99 -----EEAGRLRSKMTQMOIELLIQSQLPVEPEMIRN-----GVOSAV-- 139
Db 720 DGAQVNGIOPPEEISRLREEELRSHQVLIQSQLAEKOTVIENRSSQVSGMSQALATC 779
Qy 140 -----EQAVV----- 145
Db 780 SPRDAAEQVELKQELSAKSQCSQSLEITRLQTENRELQRAETLAKSVPVGESELVT 839
Qy 146 -----CVSLKKEYENLKEARKASGEVAKLKRDLFSSRSKLTQVYSELQAKEL 195
Db 840 AAKITDVGEVLSSALQETKELKNEKIALKSEERTSIQQLDSSNSTIAIQLQTERDKLYEV 899
Qy 196 KSAQKD-----LQSADKEIMSLKKL 216

RESULT 28

A55913

Query Match 14.7%; Score 156.5; DB 2; Length 1138;
Best Local Similarity 24.7%; Pred. No. 0.16; Mismatches 58; Conservative 45; Mismatches 73; Indels 59; Gaps 9;
Matches 66; Conservative 53; Mismatches 78; Indels 131; Gaps 9;

Qy 71 GKAEMLCSTLKKQMKYLFQQQDE-----TKQAK----- 98
Db 660 REQDQOLEELKQVQSTLKQNEQDQIATVQHQAKQHQDQYVNLKVOLGKDHHQGSHS 719
Qy 99 -----EEAGRLRSKMTQMOIELLIQSQLPVEPEMIRN-----GVOSAV-- 139
Db 720 DGAQVNGIOPPEEISRLREEELRSHQVLIQSQLAEKOTVIENRSSQVSGMSQALATC 779
Qy 140 -----EQAVV----- 145
Db 780 SPRDAAEQVELKQELSAKSQCSQSLEITRLQTENRELQRAETLAKSVPVGESELVT 839
Qy 146 -----CVSLKKEYENLKEARKASGEVAKLKRDLFSSRSKLTQVYSELQAKEL 195
Db 840 AAKITDVGEVLSSALQETKELKNEKIALKSEERTSIQQLDSSNSTIAIQLQTERDKLYEV 899
Qy 196 KSAQKD-----LQSADKEIMSLKKL 216

RESULT 29

A55913

Query Match 14.7%; Score 156.5; DB 2; Length 1138;
Best Local Similarity 24.7%; Pred. No. 0.16; Mismatches 58; Conservative 45; Mismatches 73; Indels 59; Gaps 9;
Matches 66; Conservative 53; Mismatches 78; Indels 131; Gaps 9;

Qy 71 GKAEMLCSTLKKQMKYLFQQQDE-----TKQAK----- 98
Db 660 REQDQOLEELKQVQSTLKQNEQDQIATVQHQAKQHQDQYVNLKVOLGKDHHQGSHS 719
Qy 99 -----EEAGRLRSKMTQMOIELLIQSQLPVEPEMIRN-----GVOSAV-- 139
Db 720 DGAQVNGIOPPEEISRLREEELRSHQVLIQSQLAEKOTVIENRSSQVSGMSQALATC 779
Qy 140 -----EQAVV----- 145
Db 780 SPRDAAEQVELKQELSAKSQCSQSLEITRLQTENRELQRAETLAKSVPVGESELVT 83

QY	178	RSKLOT-----VSELDOAKLLEKSAKDLQSADKEIMSLKKLITMQL220	Db	1375	RTKYETDAIQTTEELEEKKL--AQR-LQDSEGVENNAKCASTLE 1418
RESULT	17	myosin heavy chain, skeletal muscle, embryonic - rat A24922	RESULT	18	myosin heavy chain II - Acanthamoeba castellanii A27224
N;Contains:	myosin ATPase (EC 3.6.1.32)	N;Contains: myosin ATPase (EC 3.6.1.32)	C;Species:	Rattus norvegicus (Norway rat)	C;Species: Acanthamoeba castellanii
C;Date:	31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001	C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001	C;Accession:	A24922; A22338; B4263	C;Accession: A27224
R;Strehler, E.E.; Strehler-Page, M.A.; Perriard, J.C.; Periasamy, M.; Nadal-Ginard, B.	J. Mol. Biol. 190, 291-317, 1986	R;Hamer III, J.A.; Bowers, B.; Paterson, B.M.; Korn, E.D.	J. Cell Biol. 105, 913-925, 1987	A;Title: Complete nucleotide and deduced amino acid sequence of a mammalian myosin heavy chain gene	A;Title: Complete nucleotide sequence and deduced polypeptide sequence of a nonmuscle myosin heavy chain II
A;Reference number:	A24922; MUID:87060988	A;Reference number:	A27224; MUID:87308395	A;Accession:	A;Accession: A22338
A;Accession:	A24922	A;Accession:	A27224	A;Molecule type:	A;Molecule type: DNA
A;Residues:	1-1940 <STR>	A;Residues:	1-1509 <HAM>	A;Genetics:	A;Genetics: 1-1940 <PER>
A;Cross-references:	GB:X04267; GB:X05004; NID:956658; PIDN:CAA27817.1; PIDN:91619328	A;Cross-references:	GB:Y00624; GB:M12702; GB:M12703; GB:M19549; NID:95585; PIDN:CAA6646	A;Introns:	A;Introns: 1-1940 <PER>
R;Strehler, E.E.; Mandavi, V.; Periasamy, M.; Nadal-Ginard, B.	J. Biol. Chem. 260, 468-471, 1985	R;Periasamy, M.; Wido, R.M.; Strehler-Page, M.A.; Strehler, E.E.; Nadal-Ginard, B.	J. Biol. Chem. 260, 15856-15862, 1985	A;Title: Intron positions are conserved in the 5' end region of myosin heavy-chain genes	A;Title: Characterization of cDNA and genomic sequences corresponding to an embryonic myosin heavy chain
A;Title:	A;Title: Characterization of cDNA and genomic sequences corresponding to an embryonic myosin heavy chain	A;Reference number:	A22338; MUID:86059474	A;Status:	A;Status: preliminary
A;Accession:	A22338	A;Accession:	A22338	A;Molecule type:	A;Molecule type: DNA
A;Residues:	1-168 <STR>	A;Residues:	1-1509 <HAM>	A;Cross-references:	A;Cross-references: GB:L00370; GB:M10135; NID:9205580; PIDN:AAA41655.1; PIDN:9554476
A;Cross-references:	GB:L00346; NID:9205573; PIDN:AAA41652.1; PIDN:9205574	A;Cross-references:	GB:Y00624; GB:M12702; GB:M12703; GB:M19549; NID:95585; PIDN:CAA6646	A;Introns:	A;Introns: 1-168 <STR>
A;Experimental source:	clone pHNC-72	A;Experimental source:	clone pHNC-72	C;Superfamily:	C;Superfamily: myosin heavy chain
C;Genetics:	A;Note: the list of intron positions may be incomplete	C;Genetics:	A;Note: the list of intron positions may be incomplete	C;Key words:	C;Key words: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleic acid
C;Superfamily:	myosin heavy chain; myosin motor domain homology	C;Superfamily:	myosin heavy chain; myosin motor domain homology	F;92-775/Domain:	F;92-775/Domain: myosin motor domain homology <MM07>
C;Keywords:	actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle coiled coil	C;Keywords:	actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleic acid	F;182-189/Region:	F;182-189/Region: nucleotide-binding motif A (P-loop)
F;89-977/Domain:	myosin motor domain homology <MM07>	F;89-977/Domain:	myosin motor domain homology <MM07>	F;594-576/Region:	F;594-576/Region: actin binding #status predicted
F;179-186/Region:	nucleotide-binding motif A (P-loop)	F;179-186/Region:	nucleotide-binding motif A (P-loop)	F;600-682/Region:	F;600-682/Region: actin binding #status predicted
F;549-586/Region:	actin binding #status predicted	F;549-586/Region:	actin binding #status predicted	F;848-1277/Domain:	F;848-1277/Domain: hinge <HIN>
F;840-1940/Domain:	coiled coil #status predicted	F;840-1940/Domain:	coiled coil #status predicted	F;1248-1482/Domain:	F;1248-1482/Domain: hinge <HIN>
F;840-1280/Region:	S2	F;840-1280/Region:	S2	F;483-1509/Domain:	F;483-1509/Domain: carboxyl-terminal <CBT>
F;1281-1940/Region:	light meromyosin	F;1281-1940/Region:	light meromyosin	F;133/Modified site:	F;133/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F;130/Modified site:	N6,N6,N6-trimethyllysine (Lys) #status predicted	F;130/Modified site:	N6,N6,N6-trimethyllysine (Lys) #status predicted	F;188/Binding site:	F;188/Binding site: ATP (Lys) #status predicted
F;185/Binding site:	ATP (Lys) #status predicted	F;185/Binding site:	ATP (Lys) #status predicted	F;188/Binding site:	F;188/Binding site: ATP (Lys) #status predicted
F;695-706/Active site:	Cys #status predicted	F;695-706/Active site:	Cys #status predicted	F;188/Binding site:	F;188/Binding site: ATP (Lys) #status predicted
Query Match	14.5%	Score 154.5; DB 1; Length 1509;	Query Match	14.5%	Score 154.5; DB 1; Length 1509;
Best Local Similarity	25.8%	Pred. No. 0.28;	Best Local Similarity	25.8%	Pred. No. 0.28;
Matches	69;	Conservative	52;	Mismatches	91;
Db	894	DKLERDAALAKITDKITDKLEGKADELNDNALLQQKVAGLEBLQETISASNDILEKRKLE 953	Db	894	DKLERDAALAKITDKITDKLEGKADELNDNALLQQKVAGLEBLQETISASNDILEKRKLE 953
QY	5	NKLFFDLAQEEENNVDREFLKNEEDNVRAQLSQKD-----KIKRDSQ 46	QY	5	NKLFFDLAQEEENNVDREFLKNEEDNVRAQLSQKD-----KIKRDSQ 46
Db	954	AEGKGLKASLEEERNRKALQEAKTRVESNERELODQYDEAAAHDSLKRKEEDISRLR 1013	Db	954	AEGKGLKASLEEERNRKALQEAKTRVESNERELODQYDEAAAHDSLKRKEEDISRLR 1013
QY	93	ETKQOQEAEGR---LRSKAKTMEIELLIQSQLEPEV-EEMIRDAGVGOSAVEQJAVCV 147	QY	93	ETKQOQEAEGR---LRSKAKTMEIELLIQSQLEPEV-EEMIRDAGVGOSAVEQJAVCV 147
Db	1014	ETKDLAADAENSETLRSLKLNTERGADDVNRNELDVATKLQLRKTTSLEELAQTRA 1073	Db	1014	ETKDLAADAENSETLRSLKLNTERGADDVNRNELDVATKLQLRKTTSLEELAQTRA 1073
QY	148	SLKKEYEENLKEARKASGEVADKLRLDFSSRSRKLQTVYSELDQAKLELKAQ--KDLQ- 203	QY	148	SLKKEYEENLKEARKASGEVADKLRLDFSSRSRKLQTVYSELDQAKLELKAQ--KDLQ- 203
Db	1074	QLEEE----KSGKEKASSKAKLQGQLEDARSEWVSDLSKLSUSAESKLTKAKDQRDLDE 1129	Db	1074	QLEEE----KSGKEKASSKAKLQGQLEDARSEWVSDLSKLSUSAESKLTKAKDQRDLDE 1129
QY	204	-----SADKIMSKRKLTMLQ 220	QY	204	-----SADKIMSKRKLTMLQ 220
Db	1130	QLEDERTVRANVDKOKKALEAKLTLE 1156	Db	1130	QLEDERTVRANVDKOKKALEAKLTLE 1156
RESULT	19	B75150	RESULT	19	B75150
Db	1204	LAEQIDNLQRYKQKLEKEKFSEPKLEDDLSSVE-----SVSKSKANLERCRTVEDQ 1256	Db	1204	LAEQIDNLQRYKQKLEKEKFSEPKLEDDLSSVE-----SVSKSKANLERCRTVEDQ 1256
QY	84	MYKLEQQDDETRQA-----QBEAGRURSKMKTMEQIELL---QSQLPEVEM 128	QY	84	MYKLEQQDDETRQA-----QBEAGRURSKMKTMEQIELL---QSQLPEVEM 128
Db	1257	LSEARKNEVKYORSLSLTQSKRQLEAGELSRQPEKEKESTIVSOLSRSKQAFQTLQEEF 1316	Db	1257	LSEARKNEVKYORSLSLTQSKRQLEAGELSRQPEKEKESTIVSOLSRSKQAFQTLQEEF 1316
QY	129	IRDMGVGQSQATEQLAVY-----CVSLKEYENLKEARKASGEVADKLRLDFSSRSK 181	QY	129	IRDMGVGQSQATEQLAVY-----CVSLKEYENLKEARKASGEVADKLRLDFSSRSK 181
Db	1317	KROLEENKAKNHALAHALQSSRHDCCDLREOEYEEOBGKAELRALSKANSEVAQWRTKY 1376	Db	1317	KROLEENKAKNHALAHALQSSRHDCCDLREOEYEEOBGKAELRALSKANSEVAQWRTKY 1376
OY	182	OT---VYSELDOAKLLEKSAKDLQSADKEIMSLKKLITMQL 220	OY	182	OT---VYSELDOAKLLEKSAKDLQSADKEIMSLKKLITMQL 220

A;Accession: S12733
A;Molecule type: DNA
A;Residues: '1-106, 'E', 108-671, 'LYH', 675-857, 'A', 859-941, 'NV', 944-1123, 'A', 1125-1158, 'C',
A;Cross-references: EMBL:X52889; NID:929726; PID:CA370681; MID:929727
R;Izamauchi-Takihara, K.; Sole, M.J.; Liew, J.; Ing, D.; Liew, C.C.
Proc Natl Acad Sci U.S.A. 86, 3504-3508, 1989
A;Title: Characterization of human cardiac myosin heavy chain genes.
A;Reference number: A94224; MUID:89264452
A;Molecule type: DNA
A;Residues: '1-87, 'Q', 89-106, 'E', 108-177, 1325-1702, 'DR', 1705-1786, 1788-1803, 'E', 1804-1935
PCC. Natl. Acad. Sci. U.S.A. 86, 7416-7417, 1989
A;Reference number: A95226
A;Contents: annotation; erratum
R;Kurabayashi, M.; Tsuchimochi, H.; Komuro, I.; Takaku, F.; Yazaki, Y.
J. Clin. Invest. 82, 524-531, 1988
A;Residues: 1412-1518, 'R', 1520-1574, 'NV', 1577-1935 <KUR>
A;Cross-references: GB:MB21655
A;Note: the authors translated the codon AGC for residue 108 as Arg
R;Richter, P.; Umada, P.K.; Levin, J.E.; Vosberg, H.P.
A;Title: Partial characterization of the human beta-myosin heavy-chain gene which is exp
A;Reference number: A24997; MUID:87030293
A;Molecule type: DNA
A;Residues: 682-721, 915-1112, 1854-1935 <LIC>
A;Cross-references: GB:X04627
R;Saez, L.J.; Gianola, K.W.; McNally, E.M.; Feghali, R.; Eddy, R.; Shows, T.B.; Leinwand
Nucleic Acids Res. 15, 5443-5459, 1987
A;Title: Human cardiac myosin heavy chain genes and their linkage in the genome.
A;Reference number: A95669; MUID:87260010
A;Accession: A27858
A;Molecule type: DNA
A;Residues: '1854-1865, 'A', 1867-1935 <SAE>
A;Cross-references: GB:X05631; NID:934643; PID:CAA29119_1; MID:934644
R;Biederich, K.W.; Eisele, T.; Ried, T.; Jaenische, T.; Lichter, P.; Vosberg, H.P.
Hum. Genet. 81, 214-220, 1989
A;Title: Isolation and characterization of the complete human beta-myosin heavy chain ge
A;Reference number: I54254; MUID:89154425
A;Status: translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 653-720 <RRSS>
A;Cross-references: GB:M27636; NID:9179511; PIDN:AAA79019_1; PID:9601916
R;Robe, E.;
submitted to the EMBL Data Library, January 1989
A;Reference number: S12458
A;Accession: S12458
A;Molecule type: mRNA
A;Residues: '785-1076, 'E', 1078-1123, 'A', 1125-1702, 'DE', 1705-1935 <BOB>
A;Cross-references: EMBL:X51591; NID:929467; PID:CA35940_1; MID:929468
R;Robe, E.; Buchberger-Seidl, A.; Braun, T.; Singh, S.; Goedde, H.W.; Arnold, H.H.
Eur. J. Biochem. 189, 55-65, 1990
A;Title: Identification of three developmentally controlled isoforms of human myosin hea
A;Reference number: S09331; MUID:90235862
A;Accession: S09331
A;Molecule type: mRNA
A;Residues: '785-830, 'X', 832-900, 'X', 902-970, 'X', 972-1040, 'X', 1042-1076, 'E', 1078-1110, 'X'
, 1602-1670, 'X', 1672-1702, 'DE', 1705-1740, 'X', 1742-1810, 'X', 1812-1935 <BOW>
A;Cross-references: EMBL:X51591
R;Jandreski, M.A.; Liew, C.C.
Hum. Genet. 76, 47-53, 1987
A;Title: Construction of a human ventricular cDNA library and characterization of a beta
A;Reference number: S02229; MUID:87192738
A;Accession: S02229
A;Molecule type: mRNA
A;Residues: 1393-1702, 'DR', 1705-1935 <JAN>

A;Cross-references: EMBL:X06976; NID:934860; PIDN:CA30039_1; PID:9825694
R;Saez, L.; Leinwand, L.A.
Nucleic Acids Res. 14, 2951-2969, 1986
A;Title: Characterization of diverse forms of myosin heavy chain expressed in adult h
A;Reference number: A93616; MUID:86176778
A;Accession: B23767
A;Molecule type: mRNA
A;Residues: 'LLGGELASG', 1311-1312, 'G', 1314-1355, 'R', 1357-1358, 'GD', 1361-1438, 'LO', 14
A;Note: the first ten codons of the sequence figure show the reverse complementary st
C;Genetics:
A;Gene: GDB:MYH7
A;Cross-references: GDB:120215; OMIM:160760
A;Map position: 14q12-4q12
A;Introns: 67/3; 115/3; 168/2; 213/3; 244/3; 266/1; 299/1; 333/3; 380/1; 419/3
24/3; 1390/2; 1451/3; 1507/1; 1548/3; 1553/3; 1719/3; 1761/3; 1853/3; 1885/3; 1930/3
C;Superramyl: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; cardiac muscle; coiled coil; heart; hydrolase; methyl
F:88-765(Domain: myosin motor domain homology <MM00>
F:778-885(Region: nucleotide-binding motif A (P-loop)
F:548-685(Region: actin binding #status predicted
F:655-677(Region: actin binding #status predicted
F:839-1935(Domain: coiled coil #status predicted <COT>
F:1280-1935(Region: light meromyosin
F:129/Modified site: No, N6,N6-trimethyllysine (Lys) #status predicted
F:184/Binding site: ATP (Lys) #status predicted
F:695,705/Active site: Cys #status predicted

Query Match Best Local Similarity 14.3%; Score 152.5; DB 1; Length 1935;
Matches 61; Conservative 60; Mismatches 88; Indels 89; Gaps 9;
QY 1 RTIINKLFLDAQEEVNLDR-----EFLK----- 25
Db 1129 RAVKEKLRDSLSELEERFEAGGATSVQLEMNKRAFAEQKMRDLEAFATLQHEAT 1188
QY 26 -----NELDNVRAQLSQRDKERDSQVITDLTDLBERNATVVSQQA 69
Db 1189 AAALRKKHADSVALELGEOIDNLORVKOLEKEKSEFKLELDVTTSNMQ-----IIKA 1241
QY 70 LGAEAMCSTLKQMKVLEQQETKQAEQEARLRSMT-----MEIELLQSQ 121
Db 1242 KANLEKMCRTLDQMENHRSKABETORSVNDLTSQRALKTENGELSRLQDEKEALI-SQ 1300
QY 122 LP-----EVEMIRDMGVGQSAYEQLAVCVSISKKEVENKEARKASGEV 166
Db 1301 LTGKGKLYTYQOLEDKRLQEEVKAKNALHQASRCDLUREQEETAKAELQV 1360
QY 167 ADKLRKDLFSSRSKLTQ---VSELQAKLELSAQDLSKQADKETMSKKLTMQ 220
Db 1361 LSKANSEVAQWRIKYETDIAQTEELERAKKL-AQR-LQEEAVEAVNAKCSLE 1415
RESULT 23
S21801 myosin heavy chain, neuronal [similarity] - rat
N;Alternate names: myosin II
N;Species: Rattus norvegicus (Norway rat)
C;Sequence: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 19-Jan-2001
C;Accession: S21801; PN0013; S18134
R;Sun, W.; Chantler, P.D.
J. Mol. Biol. 224, 1185-1193, 1992
A;Title: Cloning of the cDNA encoding a neuronal myosin heavy chain from mammalian br
A;Reference number: S21801; MUID:92255856
A;Accession: S21801
A;Molecule type: mRNA
A;Residues: 1-1999 <SUN>
A;Cross-references: EMBL:X62659
R;Sun, W.; Chantler, P.D.
Biophys. Res. Commun. 175, 244-249, 1991
A;Title: A unique cellular myosin II exhibiting differential expression in the cerebr

A; Reference number: P00013; MUID:91151356
A; Accession: P00013
A; Molecule type: mRNA
A; Residues: 1914-1998, 'I' <SU2>
A; Experimental source: brain
C; Superfamily: myosin heavy chain: myosin motor domain homology
C; Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; nucleotide
F; 84-763;/domain: myosin motor domain homology <MMOT>
F; 171-181;/Region: nucleotide-binding motif A (P-loop)
F; 541-575;/Region: actin binding #status predicted
F; 653-675;/Region: actin binding #status predicted
F; 1916/Binding site: phosphate (Ser) (covalent) #status predicted
F; 1943/Binding site: phosphate (Ser) (covalent) #status predicted
F; 1277-1999/Region: light meromyosin
F; 180-818/Binding site: ATP (Lys) #status predicted
F; 693-703/Active site: Cys #status predicted
F; 1916/Binding site: phosphate (Ser) (covalent) #status predicted
F; 1943/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match^h 14.3%; Score 152.5; DB 1; Length 1999;
Best Local Similarity 20.7%; Pred. No. 0.49; Matches 54; Conservative 54; Mismatches 88; Indels 65; Gaps 6;

Qy 11 LAQEENNVIDREFLKNEQNRAQLSQKDEKE-----RDSQVITDTLDTLE----
Db 789 LEQEENKVIRALAQL--ELSQVRQIDRRIQKEREFENVRKNORALDSMSAEEAKG 845
Qy 58 -----ERNATVVSQOALGKRAEMLSTLKKOMYLEQQDDETKEQEEAGRRLRM 108
C;Keywords: myosin heavy chain 3, muscle - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 13-Feb-1998
C;Accession: C35815
R;Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.
Genes Dev. 4, 885-895, 1990
A;Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion t
A;Reference number: A35015; MUID:90346288
A;Accession: D35815
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1175 <COL>
A;Cross-references: EMBL:X53155
A;Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for resi
C;Genetics:
A;Gene: FlyBase:Mhc
A;Cross-references: FlyBase:FBgn0002741
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP

RESULT 24

C35815

myosin heavy chain 3, muscle - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 20-Jun-2000
C;Accession: C35815
R;Collier, V.L.; Kronert, W.A.; O'Donnell, P.T.; Edwards, K.A.; Bernstein, S.I.
Genes Dev. 4, 885-895, 1990
A;Title: Alternative myosin hinge regions are utilized in a tissue-specific fashion that
A;Reference number: A35015; MUID:90346288
A;Accession: C35815
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1175 <COL>
A;Cross-references: EMBL:X53155; NID:68219; PIDN:CAA7308_1; PDB:92546935
A;Note: the authors translated the codon TGC for residue 649 as Lys, and AAG for residue
C;Genetics:
A;Gene: FlyBase:Mhc
A;Cross-references: FlyBase:FBgn0002741
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: ATP

Query Match 14.3%; Score 152; DB 2; Length 1175;
Best Local Similarity 23.9%; Pred. No. 0.3; Matches 62; Conservative 49; Mismatches 84; Indels 64; Gaps 9;

Qy 11 LAQEENNVIDREFLKNEQNRAQLSQKDEKE-----RDSQVITDTLDTLE---- 57
Db 789 LEQEENKVIRALAQL--ELSQVRQIDRRIQKEREFENVRKNORALDSMSAEEAKG 845
Qy 58 -----ERNATVVSQOALGKRAEMLSTLKKOMYLEQQDDETKEQEEAGRRLRM 108
C;Keywords: myosin heavy chain 1, muscle - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Accession: C35815

RESULT 26

A35015

myosin heavy chain 1, muscle - fruit fly (Drosophila melanogaster) (fragment)

Qy 163 SGEVADKLRFSSRSKQTVVSBDQ-----AKL--ELKSAQD 201
Db 906 R-BOLGJSERRANALQNLSEESRTLQCDGRRQAEQ----ELADAHQELNEVSQ 957
Qy 202 LQSADKEIMSLKKKLTMLQ 220
Db 1014 AQTOEKLRALEQQIKEQ 1032

Qy 11 LAQEENNVIDREFLKNEQNRAQLSQKDEKE-----RDSQVITDTLDTLE---- 57
Db 789 LEQEENKVIRALAQL--ELSQVRQIDRRIQKEREFENVRKNORALDSMSAEEAKG 845
Qy 58 -----ERNATVVSQOALGKRAEMLSTLKKOMYLEQQDDETKEQEEAGRRLRM 108
C;Keywords: myosin heavy chain 1, muscle - fruit fly (Drosophila melanogaster) (fragment)
C;Species: Drosophila melanogaster
C;Accession: C35815

C;date: 12-Oct-1989 #sequence_revision 31-dec-1993 #text_change 02-Feb-2001
 C;Accession: B32491
 R;George, E.L.; Ober, M.B.; Emerson Jr., C.P.
 Mol. Cell. Biol. 9, 2957-2974, 1989
 A;Title: functional domains of the Drosophila melanogaster muscle myosin heavy-chain gene
 A;Accession: B32491
 A;Status: preliminary
 A;Molecule type: DNA; mRNA
 A;Residues: 1-2411 <GEO>
 A;Cross-references: GB:M61229; GB:M27194
 C;Genetics:
 A;Gene: FlyBase:Mhc
 A;Cross-references: FlyBase:FBgn0002741
 C;Superfamily: myosin heavy chain; myosin motor domain homology
 C;Keywords: ATP; nucleotide binding; p-loop
 F;227-234/Region: nucleotide-binding motif A (P-loop)
 Query Match 14.3%; Score 152; DB 2; Length 2411;
 Best Local Similarity 23.9%; Pred. No. 0.63; Mismatches 84; Indels 64; Gaps 9;
 Matches 62; Conservative 49; Atypical 10; Status atypical <MMO>
 QY 11 LAQBERENVIDREFLKNEDLNVRQLSQDKEK-----RDSQVIIIDLRTDTE---- 57
 Db 1999 LEQEENKVLRQL---ELSQVQRQIDRRIQEKFERNTRKHNORALDSMQASLEAEKG 2055
 QY 58 -----ERNATVVSQOALGKRAEMCSTLKKOMYIEQQDETQKAQEEGRRLRM 1018
 Db 2056 KAEALRMKKKLEADINELEIADHANKANAEAKNIKRYQQQLKDQTAALEEEFORARODA 2115
 QY 109 KTMPOIEL-----LLQSLPEVEMIIRMGVGOSAVEQLAVYCISLKEYENKEARKA 152
 Db 2116 R-SQOLGTSERRANALQNLQEEESRILQEADGRGRQAO-----ELADAHEPDNEVSQ 2167
 QY 163 SGEVADKLKDLSRSRKLQTVSELDQ-----AKL--ETKSAQKD 201
 Db 2168 NASISAARK---LESELOQTLSDDELINNEAKKANSEEAKKANVDAARLADLRAEQDH 2223
 QY 202 LQSADEKREIMSLKKLUTMLQ 220
 Db 2224 AQTOEKLRLKALEQOIKELO 2242

RESULT 30
 T17272 hypothetical protein DKFZp44B0435.1 - human
 C;Species: Homo sapiens (man)
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 01-Dec-2000
 C;Accession: T17272; TA6451; A36881
 R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, September 1999
 A;Reference number: 218723
 A;Accession: T17272
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1780 <POU>
 A;Cross-references: EMBL:AL117496
 A;Experimental source: adult testis; clone DKFZp44B0435
 R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, January 2000
 A;Accession: T46451
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 557-1136, 'C', 1138-1608, 'K', 1610-1780 <AAA>
 A;Cross-references: EMBL:AL137392
 A;Experimental source: adult testis; clone DKFZp4341152
 R;Westendorf, J.M.; Rao, P.N.; Gerace, L.
 Proc. Natl. Acad. Sci. U.S.A. 91, 714-718, 1994
 A;Title: Cloning of cDNAs for M-phase phosphoproteins recognized by the MPM2 monoclonal

A;Reference number: A36881; MUID:94119956
 A;Accession: A36881
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1215-1361, 'E', 1263-1418, 'S', 1420-1608, 'K', 1610-1780 <WES>
 A;Cross-references: GB:JL782; MUID:929328; PID: AAC77542.1; PID: 9592329
 C;Genetics:
 A;Note: DKFZp434B0435.1; DKFZp4341152.1
 C;Keywords: phosphoprotein
 Query Match 14.2%; Score 151.5; DB 2; Length 1780;
 Best Local Similarity 21.3%; Pred. No. 0.49; Mismatches 84; Indels 39; Gaps 6;
 Matches 50; Conservative 62; Atypical 10; Status atypical <MMO>
 QY 22 EFLKNEDLNVRQL-SQD-----KEK-----RDSQVIIIDLRTDTE---- 62
 Db 1039 EELSOQEIKLQEAEVKGYKQONNRLKEKEKNODDLKKRKTQLQKLEKESILKIE 1098
 QY 63 ---WVSQOALGKRAEMCSTLKKOMYIEQQDETQKAQEEGRRSKMTMBOIELIQ 119
 Db 1093 IQHVEGKALSELTTQGYCYKAKIKEFILEQVKVERSHSAKLEQDILEKESILKIE 1158
 QY 120 SOLPVEEEMIRDGMVGOSAVEQLAVYCISLKEYENL-----KARAKASGE 165
 Db 1159 RNLKEFOEHLQD--SVKNTKDLNVKEILKEETIOTLNQNLDQMKHLIQLKEEEETNRQ 1215
 QY 165 VADKURKDFFSRSKLQTYSELDQAKLELKSQADKELMSLKKLTMQ 220
 Db 1215 ETEKLUKEESSASSARTONIKADQKKEBYADEKLTADKKOIKQKQEVSMR 1270

RESULT 31
 S54871 M protein - Streptococcus sp.
 C;Species: Streptococcus sp.
 C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 26-Aug-1999
 C;Accession: S54871
 C;Author: Podbielski, A.; Melzer, B.
 submitted to the EMBL Data Library, June 1991
 A;Reference number: S54871
 A;Accession: S54871
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-532 <POD>
 A;Cross-references: EMBL:X60097; MUID:9840905; PID:CAA42693.1; PID:9840906
 C;Superfamily: M5 protein

Query Match 14.2%; Score 151; DB 2; Length 532;
 Best Local Similarity 23.0%; Pred. No. 0.15; Mismatches 93; Indels 62; Gaps 8;
 Matches 62; Conservative 52; Atypical 10; Status atypical <MMO>
 QY 9 FDLAQE-----FENVLDREFLK-----NEIDLNVRQLS----- 37
 Db 174 YDLFEELGKKLKENQDLEEKLKDFKEFYIGETLRYINSLDKLGQLNNDIDLKHLEQE 233
 QY 38 KDKIKRDSQVITDYLRTDLEERNATVVSQOALGKRAEMCSTLKKOMYIEQQDETQKA 97
 Db 234 KQKAEADRT-LEEKAKLEEEKQIISDARSQSLRDLDAASREAKKQLEYORLEEQI 292
 QY 98 QEEAGR-LRSKMKTMEQIELLQSQLPVEE-----MIRDGMVGOSAVEQLAWY 145
 Db 293 SDASRQSLRDLDAASREAKKQLEYORLEEQIISDARSQSLRDLDAASREAKKQLE 352
 QY 146 CVSLSKKEYNLKEARKKASEGEVADKLKDFFSSRSKLTQTYSELDQAKLELKSQI--KDL 202
 Db 353 LANLTAELDKVKEEKOISDASRKGLRQLRDLDAASREAKKQLEYORLEEQI 412
 QY 203 OSACK-----EIMSLKKI 216
 Db 413 EESKRLTEEKAELQAKLKEAKALKKEI 441

	RESULT 32
C;Species: Homo sapiens (man)	QY 118 LQSQLPEVEMIRDMGVGOSAVEOLAVCVSLKKEYENLKEA-----KASGEVAD- 168
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000	Db 335 KR---HLEEIKKANALAHOSARHDDCLLRRQEQQEAEKGELQRLLSKANSEVAQ 390
C;Accession: 153799	Db 391 RTKYETDAIQTEREELEAKKLQAQ--RLQDAEBHEAVNAKCASLEKTKRQLQ 441
R;Print, C.G.; Leung, E.; Harrison, J.E.; Watson, J.D.; Krissansen, G.W.	A;Title: Cloning of a gene encoding a human leukocyte protein characterised by extensive A;Reference number: 153799; MUID:94314220
A;Status: preliminary; translated from GB/EMBL/DBJ	A;Molecule type: mRNA
A;Residues: 1-1300 <RES>	A;Cross-references: GB:L25616; NID:9409465; PIDN:AA65853.1; PID:9409466
A;Genes: GDB:CG1	A;Cross-references: GDB:450341
Query Match 14.2%; Score 151; DB 2; Length 1300;	Query Match 14.2%; Score 151; DB 2; Length 1300;
Best Local Similarity 26.6%; Pred. No. 0.38; Mismatches 67; Conservative 40; Indels 64; Gaps 11;	Best Local Similarity 26.6%; Pred. No. 0.38; Mismatches 67; Conservative 40; Indels 64; Gaps 11;
Db 306 DLLKEKSGVTDALKSSKGELTLIHOLQEKDKLLAAVKEDAATKDRCKQLTQEMME 365	Db 306 DLLKEKSGVTDALKSSKGELTLIHOLQEKDKLLAAVKEDAATKDRCKQLTQEMME 365
QY 42 KRDSDQVITDILRD--TLEE-----INATAVSLSQQLQAGKAEMCSTLKKQMY--LEQ 90	QY 42 KRDSDQVITDILRD--TLEE-----INATAVSLSQQLQAGKAEMCSTLKKQMY--LEQ 90
Db 366 KERSNVWITRMKDRIGHTLEKEHNVFQNKHYQOE-----TQOMQMFKQFQREOM 415	Db 366 KERSNVWITRMKDRIGHTLEKEHNVFQNKHYQOE-----TQOMQMFKQFQREOM 415
QY 91 QDETQKQAEAGRLSKM-KMPEQIELLQSLQPEVEMIRMGVGOSAVEOLAVCVSL 149	QY 91 QDETQKQAEAGRLSKM-KMPEQIELLQSLQPEVEMIRMGVGOSAVEOLAVCVSL 149
Db 416 EAELAHIIKQENGILRPAVNTINOLE--SKOSAELNKLKRQDYA--RLVNLTEKGKL 469	Db 416 EAELAHIIKQENGILRPAVNTINOLE--SKOSAELNKLKRQDYA--RLVNLTEKGKL 469
QY 150 KREYENLKKEARKASGEVADKLRSKQIQTVSSELDOKKLEKSAQDQIQS---A 205	QY 150 KREYENLKKEARKASGEVADKLRSKQIQTVSSELDOKKLEKSAQDQIQS---A 205
Db 470 QQEEVOKKNAFOA---ATOLKVQLOBAERRWEVEVSYIRKTAEHAAQDQLQSKFVKA 525	Db 470 QQEEVOKKNAFOA---ATOLKVQLOBAERRWEVEVSYIRKTAEHAAQDQLQSKFVKA 525
QY 206 DKEIMSLKKIUT 217	QY 206 DKEIMSLKKIUT 217
Db 526 ENEVQSLHSKLQ 537	Db 526 ENEVQSLHSKLQ 537
RESULT 33	RESULT 34
S24348 myosin heavy chain, embryonic and adult skeletal muscle (clone Cemb2) - chicken (fragment)	QY 84 MKYIEQQDDE-----TKQH-QEERGRLL-----RKSMMKTMEQIELL 117
A;Reference number: S24348; MUID:92309413	Db 275 LSKIKKSEBEHORMINDLSTORARLARLTSEGEYSRQEVEKDALISQLSRGKQAOFTQOIEL 334
A;Status: nucleic acid sequence not shown	QY 118 LQSQLPEVEMIRDMGVGOSAVEOLAVCVSLKKEYENLKEA-----KASGEVAD- 168
A;Molecule type: mRNA	Db 335 KR---HLEEIKKANALAHOSARHDDCLLRRQEQQEAEKGELQRLLSKANSEVAQ 390
A;Residues: 1-955 <MOOD>	Db 391 RTKYETDAIQTEREELEAKKLQAQ--RLQDAEBHEAVNAKCASLEKTKRQLQ 441
A;Cross-references: EMBL:M74085	A;Title: Cloning of the cDNA encoding a myosin heavy chain B isoform of Xenopus nonmu-
C;Superfamily: myosin heavy chain; myosin motor domain homology	A;Status: preliminary; not compared with conceptual translation
C;Keywords: ATP; coiled coil; muscle contraction; skeletal muscle; thick filament	A;Molecule type: mRNA
Query Match 14.1%; Score 150.5; DB 2; Length 955;	A;Residues: 1-1992 <BHA>
Best Local Similarity 23.9%; Pred. No. 0.29; Mismatches 56; Conservative 47; Indels 51; Gaps 8;	A;Cross-references: GB:L09740; NID:9214623; PIDN:AAA49915.1; PID:9214624
Db 222 LGEQIDNLRQVKQLEKEKSELKMEIDDLASME-----SVSKAKANLERMCRTLEDQ 274	A;Experimental source: XNC cells
Query Match 14.1%; Score 150.5; DB 2; Length 955;	A;Note: sequence extracted from NCBI backbone (NCBIP:1228722)
Best Local Similarity 23.9%; Pred. No. 0.29; Mismatches 56; Conservative 47; Indels 51; Gaps 8;	
Db 222 LGEQIDNLRQVKQLEKEKSELKMEIDDLASME-----SVSKAKANLERMCRTLEDQ 274	
RESULT 35	RESULT 35
A47297 myosin heavy chain form B, nonmuscle - African clawed frog	QY 128 MIRDGVGOSAVEOLAVCVSLKKEYENLKEA-----KASGEVADKLRFDFSSRSRKQIVYE 187
C;Species: Xenopus laevis (African clawed frog)	Db 337 LERIVGTIOLER-----LKREYKSIKEVER-----EKLRL-ELEEEERLKIKTFDE 382
C;Date: 03-Feb-1994 #sequence_revision 06-Sep-1996 #text_change 13-Feb-1998	QY 188 L-----DQAKL-EIJKSACKDLSADKEDMSKLKKRLTMQ 220
C;Accession: S24348	Db 383 VKKLEEEKEKLTERKLNSLNKEQEELEIQRANKNKKIERIK 422
J; Mol. Biol. 225, 1143-1151, 1992	
A;Title: Analysis of the chicken fast myosin heavy chain family. Localization of isoform	
A;Reference number: S24348; MUID:92309413	
A;Accession: S24348	
A;Status: nucleic acid sequence not shown	
A;Molecule type: mRNA	
A;Residues: 1-955 <MOOD>	
A;Cross-references: EMBL:M74085	
C;Superfamily: myosin heavy chain; myosin motor domain homology	
C;Keywords: ATP; coiled coil; muscle contraction; skeletal muscle; thick filament	
Query Match 14.1%; Score 150.5; DB 2; Length 955;	
Best Local Similarity 23.9%; Pred. No. 0.29; Mismatches 56; Conservative 47; Indels 51; Gaps 8;	
Db 222 LGEQIDNLRQVKQLEKEKSELKMEIDDLASME-----SVSKAKANLERMCRTLEDQ 274	
Query Match 14.1%; Score 150.5; DB 2; Length 955;	
Best Local Similarity 23.9%; Pred. No. 0.29; Mismatches 56; Conservative 47; Indels 51; Gaps 8;	
Db 222 LGEQIDNLRQVKQLEKEKSELKMEIDDLASME-----SVSKAKANLERMCRTLEDQ 274	
RESULT 35	RESULT 35
A47297 myosin heavy chain form B, nonmuscle - African clawed frog	QY 128 MIRDGVGOSAVEOLAVCVSLKKEYENLKEA-----KASGEVADKLRFDFSSRSRKQIVYE 187
C;Species: Xenopus laevis (African clawed frog)	Db 337 LERIVGTIOLER-----LKREYKSIKEVER-----EKLRL-ELEEEERLKIKTFDE 382
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 02-Feb-2001	QY 188 L-----DQAKL-EIJKSACKDLSADKEDMSKLKKRLTMQ 220
C;Accession: A47297; A55441	Db 383 VKKLEEEKEKLTERKLNSLNKEQEELEIQRANKNKKIERIK 422
R;Briant-Dey, N.; Adelstein, R.S.; Dawid, I.B.	
Proc. Natl. Acad. Sci. U.S.A. 90, 2856-2859, 1993	
A;Title: Cloning of the cDNA encoding a myosin heavy chain B isoform of Xenopus nonmu-	
A;Status: preliminary; not compared with conceptual translation	
A;Molecule type: mRNA	
A;Residues: 1-1992 <BHA>	
A;Cross-references: GB:L09740; NID:9214623; PIDN:AAA49915.1; PID:9214624	
A;Experimental source: XNC cells	
A;Note: sequence extracted from NCBI backbone (NCBIP:1228722)	

R; Kelley, C.A.; Oberman, F.; Yisraeli, J.K.; Adelstein, R.S.
J. Biol. Chem. 270, 1395-1401, 1995
A; Title: A xenopus nonmuscle myosin heavy chain isoform is phosphorylated by cyclin-p34cdc2 kinase
A; Reference number: A55441; MUID:95138137
A; Status: preliminary
A; Molecule type: protein
A; Residues: 198-232 <KEL>
C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Keywords: nucleotide binding; P-loop
F; 88-787/Domain: myosin motor domain homology <MMOT>
F; 178-185/Region: nucleotide-binding motif A (P-loop)

Query Match_h 14.1%; Score 150.5; DB 2; Length 192;
Best Local Similarity 22.9%; Pred. No. 0.63; Mismatches 85; Indels 53; Gaps 9;
Matches 58; Conservative 57; Mismatches 85; Indels 53; Gaps 9;

Qy 4 INKLEFLDIAEEEENV-----LDREF-----LNEDNVRQLSQK 38
Db 1093 IEELKLQAKKEELQAAALARGDEEVLOQNNTLKVRELAQIABLEDELESERASRKA 1152

Qy 39 DKEKRDSQVITDLRTDLEERNATVSLQOALGKAEMLCSTLKKOMYLEQQDTKQAO 98
Db 1153 EKOKRDSEELALKTELETDITPAQQELTRREQEVAELRSI-----EBTRNHE 1206

Qy 99 EEAAGRURSKMKT-MEQIELLIQSQPEVEEMIRDGMVGOSAVE---QLAVYCYSILK-E 152
Db 1207 AQIQEMRQRQATALEE---LSEQLEOAARKFKVNLEKNKOSLEDNKELEATEVKSLOQM 1262

Qy 153 YENIKEARAKASGEV-----ADKLRLQFSSPSKIQPVYSELQDQAKELSAQDQ 203
Db 1263 AESEYRKRLKLEGQVOELHAKVLLEGDRLLRADMVEKSSKLQ---NELENVSSLLEEEAKGT 1319

Qy 204 SADKEIMSLKKK 216
Db 1320 KLAKDQVASMESQL 1332

RESULT 36
JC5837
364K Golgi complex-associated protein - rat
C; Species: Rattus norvegicus (Norway rat)
C; Accession: JC5837
C; Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 20-Jun-2000
R; Toki, C.; Fujiwara, T.; Sohda, M.; Hong, H.S.; Misumi, Y.; Ichihara, Y.
Cell Struct. Funct. 22, 565-577, 1997
Article: Identification and characterization of rat 364-kDa Golgi-associated protein rec
A; Reference number: JC5837; MUID:98093490
A; Accession: JC5837
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-3187 <TOK>
A; Cross-references: DDBJ:D25543; NID:9516825; PIDN:BA05026.1; PID:9516826
C; Comment: This protein plays a role in the formation and maintenance of the characteris
F; 49-549, 624-176, 1238-1707, 1763-3114/Domain: coiled-coil leucine zipper #status predict
F; 3165-3187/Domain: membrane anchor #status predicted <MDA>

Query Match 14.1%; Score 150.5; DB 2; Length 3187;
Best Local Similarity 19.0%; Pred. No. 1; Mismatches 58; Conservative 59; Indels 99; Gaps 7;
Matches 58; Conservative 59; Mismatches 90; Indels 99; Gaps 7;

Qy 10 DLQAQEENVLDREFLKN--ELDNVRAQLSQKDKER-----DSQVITDLRTDLEER 59
Db 1310 ELESSQKLTADLEHLKTQPELETQHVQKEEVSYLVQGQGEKEQPLTTVQTEMEO 1369

Qy 60 NATVSL-----QQAQGAEMLCSTLKKOMYLFQQQ----- 91
Db 1370 ERLIKALHQTEMQAKEHSERLKQVQECELEKKQPKELEEEAKQQLQRKQLQALISR 1429

Qy 92 -----DETQQAQEAAGRURSKM---KTMQIELLIQSQPEVEEMIRDGMVGOSAVEQLAVYCYSILKKEYENIKEAR-- 160

Db 1430 KEALKENKLSLQBQSSARDAVEHLTKSLADVQSVQVQNEKDALLGKALQERDKLT 1489
Qy 144 V-----YCVSISK----- 150
Db 1490 VEMDSKLENSOLSGSCESSUSKLAQGGTEDKEKLMKELSVRSCKIAESTEWQEKHKELQ 1549
Qy 151 KEYENIKEARAKASGEVADKLRLQFSSKQLTQYSELQDQAKLKSACKDLSQADKEIM 210
Db 1550 KEYEVILQSYENVNSNEARIQHVWESVROEQEVYAKLSSAESDKRERKQLODAEQUE 1609
Qy 211 SLKKL 216
Db 1610 EMKEKM 1615

RESULT 37
S39082 myosin heavy chain, embryonic - chicken (fragment)
C; Species: Gallus gallus (chicken)
C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 13-Aug-1999
C; Accession: S39082; S24349; A30170; S1265
R; Moore, L.A.; Arrizubietta, M.J.; Tidyanan, W.E.; Herman, L.A.; Bandman, E.
A; Description: Analysis of the chicken fast myosin heavy chain family: Localization o
A; Reference number: S39081
A; Accession: S39082
A; Molecule type: mRNA
A; Residues: 1-741 <MOO>
A; Cross-references: EMBL:M74086
A; Experimental source: clone Cemb3
R; Moore, L.A.; Arrizubietta, M.J.; Tidyanan, W.E.; Herman, L.A.; Bandman, E.
A; Title: Analysis of the chicken fast myosin heavy chain family. Localization o
A; Reference number: S24348; MUID:92309413
A; Accession: S24349
A; Molecule type: mRNA
A; Residues: 1-12,14-741 <MOO2>
A; Cross-references: EMBL:M74086
A; Experimental source: clone Cemb3
R; Labrutta, A.A.; McCarthy, J.G.; Scherzinger, C.A.; Heywood, S.M.
DNA 8, 39-50, 1989
A; Reference number: A30170; MUID:89210285
A; Accession: A30170
A; Molecule type: DNA
A; Residues: 723-741 <LAG>
A; Cross-references: GB:M24691; NID:9341219; PIDNA:AAA48950.1; PID:9531186
R; McCarthy, J.G.; Heywood, S.M.
Nucleic Acids Res. 15, 8069-8085, 1987
A; Title: A long poly(pyrimidine/polypurine tract induces an altered DNA conformation o
A; Reference number: S01265; MUID:88040428
A; Accession: S01265
A; Molecule type: DNA
A; Residues: 723-741 <MCC>
A; Cross-references: EMBL:X06251; NID:953600; PIDN:CAA29593.1; PID:963601
C; Superfamily: myosin heavy chain; myosin motor domain homology
C; Keywords: actin binding; ATP; coiled coil; muscle

Query Match 14.1%; Score 150; DB 2; Length 741;
Best Local Similarity 24.6%; Pred. No. 0.24; Mismatches 61; Conservative 46; Indels 60; Gaps 10;
Matches 61; Conservative 46; Mismatches 81; Indels 60; Gaps 10;

Qy 10 DLQAQEENVLDREFLKN--ELDNVRAQLSQKDKER-----DSQVITDLRTDLEER 69
Db 3 DLSRLEEL-----SEH-QRVQKGL--EKEKSELMKIMIDDLSNME-----SVSKA 46

Qy 70 LGKADMCLCSTLKKOMYLFQQQ----- 104
Db 47 KANLKEMCRTLEDQSEIETKEEHHORMINDNTQRARLQTAEGEYSRQVEEKDALISQ 106

Qy 105 -RSRMKTMQIELLIQSQPEVEEMIRDGMVGOSAVEQLAVYCYSILKKEYENIKEAR-- 160

Db 107 SRGKQAFQQIEELKR---HLEEEIKAKNHALAHOSARHDCLLREQYEEQEAEKGL 162
 Qy 161 ---KASGEVAD--KURKDLESSRLQTVYSELDOAKLEJKSAQKDQSADKEIMSL 212
 Db 163 QRALSKANSEVAQWRTKETDAQTTEREELLEAKKLQG---RQDAEHVEAVNAKDSL 219
 Qy 213 KKKLIMLQ 220
 Db 220 EKIQKRLQ 227

RESULT 38
 S02771 myosin heavy chain A [similarity] - Caenorhabditis elegans
 N;Contains: myosin ATPase (EC 3.6.1.32)
 C;Species: Caenorhabditis elegans
 C;Date: 31-Dec-1993 #sequence_revision 19-May-2000 #text_change 19-Jan-2001
 C;Accession: T23622; S02771
 R;Harris, B.
 A;reference number: Z19773
 A;accession: T23622
 A;status: submitted to the EMBL Data Library, August 1996
 A;reference number: Z19773
 A;accession: T23622
 A;status: translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-1992 <WIL>
 A;Cross-references: EMBL:Z78199; PIDN: CAB01576.1; GSPDB: GN00023; CESP: K12F2.1
 A;Experimental source: clone K12F2
 R;Dibb, N.J.; Maruyama, I.N.; Krause, M.; Karn, J.
 J. Mol. Biol. 205, 603-613, 1989
 A;Title: Sequence analysis of the complete *Caenorhabditis elegans* myosin heavy chain gene
 A;Reference number: S02771; MUID:891/8677
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-116,140-1992 <DB>
 A;Cross-references: EMBL:X0067; NID:96798; PIDN:CAA30856.1; PID:96799
 A;Genetics:
 A;Gene: myo-3; CESP: K12F2.1
 A;Map position: 5
 A;Intron: 46/1; 192/1; 292/1; 468/2; 1921/3
 C;Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle ca
 F;89-802/Domain: myosin motor domain homology <db>
 F;89-209/Region: nucleotide-binding motif A (P-loop)
 F;90-712/Region: actin binding #status predicted
 F;93-807/Region: actin binding #status predicted
 F;875-1982/Domain: coiled coil #status predicted <COR>
 F;875-1189/Region: S2
 F;1190-1992/Region: light meromyosin
 F;153/Modified site: N6,N6-trimethyllysine (Lys) #status predicted
 F;730,740/Active site: Cys #status predicted

Query Match 14.1%; Score 150; DB 1; Length 1992;
 Best Local Similarity 23.5%; Pred. No. 0.67; Mismatches 64; Conservative 48; Mismatches 94; Indels 66; Gaps 10;

Query Match 14.1%; Score 149; DB 2; Length 919;
 Best Local Similarity 23.1%; Pred. No. 0.34; Mismatches 61; Conservative 52; Mismatches 83; Indels 68; Gaps 9;

Db 921 NALFLSLETEKANLADAEBERNEKINLQLKATESKLSDITGQLEDQMDQERNEDLARQKKTD 980
 Qy 46 QVIRD-----LRLTLEE---RWAIVVSIQOAGKAEMLCSTKPKOMKYLEQDQD 92
 Db 981 QEQSDTTKKVQDLELSLRRAEQEKSODRNIRSQIODEMANQDRAVAKUNKEKH--QEE 1037
 Qy 93 ETKQKQEEAGRLRSKMKTMEQIELLQLQSLPVEEMI---RDMGVGQSAVEGLAVCVS 148
 Db 1038 SNRKLNEDLQSEDEPKVNHLKIRNLKGQMDDELEENIDREKRSRGDIERAKRKEV--GD 1094
 Qy 149 LKEYENLKEKARAKASGEVADKLK--DLFSSR-----SKLQTYSE----- 188

RESULT 39
 S43554 plasminogen-binding protein MLG72 - *Streptococcus* sp. (fragment)
 C;Species: *Streptococcus* sp.
 A;Variety: group G
 C;Date: 07-Sep-1994 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000
 C;Accession: S45559; S43554
 R;ben Nasr, A.; Wistedt, A.; Ringdahl, U.; Sjoerbring, U.
 Eur. J. Biochem. 222, 267-276, 1994
 A;Title: Streptokinase activates plasminogen bound to human group C and G streptococ
 A;Reference number: S45598; MUID:94291620
 A;Accession: S45599
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-472 <BE2>
 A;Cross-references: EMBL:Z232678; NID:9474769; PIDN:CAA83589.1; PID:91333838
 C;Superfamily: M5 protein

Query Match 14.0%; Score 149; DB 2; Length 472;
 Best Local Similarity 24.7%; Pred. No. 0.17; Mismatches 59; Conservative 46; Indels 40; Gaps 7; Matches 94; Mismatches 59; Conservative 46; Indels 40; Gaps 7;

Db 118 DLNQDLEERFLKDKREFYLGETRYVNEELDLKQGLNNDLKHLEQEKKQAEADDTL 176
 Qy 50 DTIJDLTLEERNATVVSQQLQALGAEMLCSTLKKQMKYLEQQDETQKQOQEEGR-LRSKM 108
 Db 177 EAERAKLKEEKQTSDasQSRQSLDASREAKKOLEAYQKLEEKQISDASRQSLRDL 236
 Qy 109 KTMOQIELLQLQSLQPEVER-----MTRDMGVGQSOAYEOLAVYCQSVLKKEYNLK 157
 Db 237 DASREAKKQLEAEYQKLEBQNKISEASRRGLRRLDASREAKKQ-----LEAHOKL 289
 Qy 158 EARKASGEVADKURKDLEFSRSRSLQTVYSELDOAKLEJKSAQKDQSADKEIMSLKKL 216
 Db 290 EONKISEASRKGLRRLDASREAKKQVERDNLTAELDKVKEEKQISDTSRKGLRRLD 348

RESULT 40
 B72765 hypothetical protein APE010 - *Aeropyrum pernix* (strain K1)
 C;Species: Aeropyrum pernix
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 02-Feb-2001
 C;Accession: B72765
 R;Kwarrabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tawa, H.; Takanaga, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.
 DNA Res. 6, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, *Aero*
 A;Reference number: A72450; MUID:99310339
 A;Accession: B72765
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-919 <KAW>
 A;Cross-references: DDJB:AP000058; NID:95103388; PIDN:BAA79020.1; PID:95103499
 A;Experimental source: strain K1
 A;Genetics:
 A;Gene: APE010
 C;Superfamily: Archaeoglobus fulgidus conserved hypothetical protein AF1032

Query Match 14.0%; Score 149; DB 2; Length 919;
 Best Local Similarity 23.1%; Pred. No. 0.34; Mismatches 61; Conservative 52; Mismatches 83; Indels 68; Gaps 9;

QY 12 AQEEENVLDR-EFLKNELDNRQAQLSOK---DREKRDSOVITLTDLEERNATVSL 65
 ::: | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 410 SEKPESVLERUDAVINDLESKARALDQEASALEAEARLVQASMLEESEGGSSARCPCVCGA 459
QY 67 QQLGKAEMCLSTLKQMKL---EQQDETQOQEEAGRRLSKWMTWQIEUJLQSOL 122
 ::: | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 470 ELPCCRAEAATRYHAEELRKAAKEAAEAKARAASRLQDKRR--RIELL-SRL 525
QY 123 PEVERMIRDNGVGOSAVEQLAVYCUSLKEYENLKEARKASGEVADKLRL----- 171
 ::: | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 526 NQLEGLRLEGF- QTPEDLAKAOKLMLRERLEELRKLENLSLEEVKNLSREVALRE 583
QY 172 -----KDLFSRSKIQ-----TIVSELDOAK 192
Db 584 AKTRALEVILQRLGIKEEAREKLKTLSSESKKLMVSAEDLATRGITAYRSIDDL- 642
QY 193 LEKSAQKDLOQADKEIMSIKKL 216
 | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 643 --LEKAREALEGVDKELSAIERRL 664

Search completed: September 4, 2002, 16:13:00
Job time: 3244 sec